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<130> 1489EUR

<160> 22

<170> PatentIn version 3.1

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<213> Clytia gregaria

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Ser Gly Ile Cys Ser Ser Asp Glu Asp Ala Glu Lys Thr Phe Lys His
145 150 155 160

Cys Asp Leu Asp Asn Ser Gly Lys Leu Asp Val Asp Glu Met Thr Arg
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Tyr Gly Asn Phe Val Pro
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35 40 45

Ala Ser Asp Asp Ile Ser Ala Lys Leu Gly Ala Thr Pro Glu Gln Thr
50 55 60

Lys Arg His Gln Asp Ala Val Glu Ala Phe Phe Lys Lys Ile Gly Met
65 70 75 80

Asp Tyr Gly Lys Glu Val Glu Phe Pro Ala Phe Val Asp Gly Trp Lys
85 90 95

Glu Leu Ala Asn Tyr Asp Leu Lys Leu Trp Ser Gln Asn Lys Lys Ser
100 105 110

Leu Ile Arg Asp Trp Gly Glu Ala Val Phe Asp Ile Phe Asp Lys Asp
115 120 125

Gly Ser Gly Ser Ile Ser Leu Asp Glu Trp Lys Ala Tyr Gly Arg Ile
130 135 140

Ser Gly Ile Cys Ser Ser Asp Glu Asp Ala Glu Lys Thr Phe Lys His
145 150 155 160

Cys Asp Leu Asp Asn Ser Gly Lys Leu Asp Val Asp Glu Met Thr Arg
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Gln His Leu Gly Phe Trp Tyr Thr Leu Asp Pro Asn Ala Asp Gly Leu
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Tyr Gly Asn Phe Val Pro
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35 40 45

Ala Ser Asp Asp Ile Cys Ala Lys Leu Gly Ala Thr Pro Glu Gln Thr
50 55 60

Lys Arg His Gln Asp Ala Val Glu Ala Phe Phe Lys Lys Ile Gly Met
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Asp Tyr Gly Lys Glu Val Glu Phe Pro Ala Phe Val Asp Gly Trp Lys
85 90 95

Glu Leu Ala Asn Tyr Asp Leu Lys Leu Trp Ser Gln Asn Lys Lys Ser
100 105 110

Leu Ile Arg Asp Trp Gly Glu Ala Val Phe Asp Ile Phe Asp Lys Asp
115 120 125

Gly Ser Gly Cys Ile Ser Leu Asp Glu Trp Lys Ala Tyr Gly Arg Ile
130 135 140

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145 150 155 160

Cys Asp Leu Asp Asn Ser Gly Lys Leu Asp Val Asp Glu Met Thr Arg
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Tyr Gly Asn Phe Val Pro
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35 40 45

Ala Ser Asp Asp Ile Cys Ala Lys Leu Gly Ala Thr Pro Glu Gln Thr
50 55 60

Lys Arg His Gln Asp Ala Val Glu Ala Phe Phe Lys Lys Ile Gly Met
65 70 75 80

Asp Tyr Gly Lys Glu Val Glu Phe Pro Ala Phe Val Asp Gly Trp Lys
85 90 95

Glu Leu Ala Asn Tyr Asp Leu Lys Leu Trp Ser Gln Asn Lys Lys Ser
100 105 110

Leu Ile Arg Asp Trp Gly Glu Ala Val Phe Asp Ile Phe Asp Lys Asp
115 120 125

Gly Ser Gly Ser Ile Ser Leu Asp Glu Trp Lys Ala Tyr Gly Arg Ile
130 135 140

Ser Gly Ile Cys Ser Ser Asp Glu Asp Ala Glu Lys Thr Phe Lys His
145 150 155 160

Cys Asp Leu Asp Asn Ser Gly Lys Leu Asp Val Asp Glu Met Thr Arg
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Tyr Gly Asp Phe Val Pro
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35 40 45

Ala Ser Asp Asp Ile Cys Ala Lys Leu Gly Ala Thr Pro Glu Gln Thr
50 55 60

Lys Arg His Arg Asp Ala Val Glu Ala Phe Phe Lys Lys Ile Gly Met
65 70 75 80

Asp Tyr Gly Lys Glu Val Glu Phe Pro Val Phe Val Asp Gly Trp Lys
85 90 95

Glu Leu Ala Asn Tyr Asp Leu Lys Leu Trp Ser Gln Asn Lys Lys Ser
100 105 110

Leu Ile Arg Asp Trp Gly Glu Ala Val Phe Asp Ile Phe Asp Lys Asp
115 120 125

Gly Ser Gly Ser Ile Ser Leu Asp Glu Trp Lys Ala Tyr Gly Arg Ile
130 135 140

Ser Gly Ile Cys Ser Ser Asp Glu Asp Ala Glu Lys Thr Phe Lys His
145 150 155 160

Cys Asp Leu Asp Asn Ser Gly Lys Leu Asp Val Asp Glu Met Thr Arg
165 170 175

Gln His Leu Gly Phe Trp Tyr Ile Leu Asp Pro Asn Ala Asp Gly Leu
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Tyr Gly Asn Phe Val Pro
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Asp Ile Asn Gly Asp Gly Lys Ile Thr Leu Asp Glu Ile Val Ser Lys
35 40 45

Ala Ser Asp Asp Ile Cys Ala Lys Leu Gly Ala Thr Pro Glu Gln Thr
50 55 60

Lys Arg His Gln Asp Ala Val Glu Ala Phe Phe Lys Lys Ile Gly Met
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Asp Phe Gly Lys Glu Val Glu Phe Pro Ala Phe Val Asp Gly Trp Lys
85 90 95

Glu Leu Ala Asn Tyr Asp Leu Lys Leu Trp Ser Gln Asn Asn Lys Ser
100 105 110

Leu Ile Arg Asp Trp Gly Glu Ala Val Phe Asp Ile Leu Asp Lys Asp
115 120 125

Gly Ser Gly Ser Ile Ser Leu Asp Glu Trp Lys Ala Tyr Gly Arg Ile
130 135 140

Ser Gly Ile Cys Arg Ser Asp Glu Asp Ala Glu Lys Thr Phe Lys His
145 150 155 160

Cys Asp Leu Asp Asn Ser Gly Lys Leu Asp Val Asp Glu Met Thr Arg
165 170 175

Gln His Leu Gly Phe Trp Tyr Thr Leu Asp Pro Asn Ala Asp Gly Leu
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Tyr Gly Asn Phe Val Pro
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35 40 45

Ala Ser Asp Asp Ile Cys Ala Lys Leu Gly Ala Thr Pro Glu Gln Thr
50 55 60

Lys Arg His Gln Asp Ala Val Glu Ala Phe Phe Lys Lys Ile Gly Met
65 70 75 80

Asp Tyr Gly Lys Glu Val Glu Phe Pro Ala Phe Val Asp Gly Trp Lys
85 90 95

Glu Leu Ala Asn Tyr Asp Leu Lys Leu Trp Ser Gln Asn Lys Lys Ser
100 105 110

Leu Ile Arg Asp Trp Gly Glu Ala Val Phe Asp Ile Phe Asp Lys Asp
115 120 125

Gly Ser Gly Ser Ile Ser Leu Asp Glu Trp Lys Ala Tyr Cys Arg Ile
130 135 140

Ser Gly Ile Cys Ser Ser Asp Glu Asp Ala Glu Lys Thr Phe Lys His
145 150 155 160

Cys Asp Leu Asp Asn Ser Gly Lys Leu Asp Val Asp Glu Met Thr Arg
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<223> Clytin mutant: 3C12 mutant

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35 40 45

Ala Ser Asp Asp Val Cys Ala Lys Leu Gly Ala Thr Pro Glu Gln Thr
50 55 60

Lys Arg His Gln Asp Ala Val Glu Ala Phe Phe Lys Lys Ile Gly Met
65 70 75 80

Asp Tyr Gly Lys Glu Val Glu Phe Pro Ala Phe Val Asp Gly Trp Lys
85 90 95

Glu Leu Ala Asn Tyr Asp Leu Lys Leu Trp Ser Gln Asn Lys Lys Ser
100 105 110

Leu Ile Arg Asp Trp Gly Glu Ala Val Phe Asp Ile Phe Asp Lys Asp
115 120 125

Gly Ser Gly Ser Ile Ser Leu Asp Glu Trp Lys Ala Tyr Gly Arg Ile
130 135 140

Ser Gly Ile Cys Arg Ser Asp Glu Asp Ala Glu Lys Thr Phe Lys His
145 150 155 160

Cys Asp Leu Asp Asn Ser Gly Lys Leu Asp Val Asp Glu Met Thr Arg
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Tyr Gly Asn Phe Val Pro
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Asp Ile Asn Gly Asp Gly Lys Val Thr Leu Asp Glu Ile Val Ser Lys
35 40 45

Ala Ser Asp Asp Ile Cys Ala Arg Leu Gly Ala Thr Pro Glu Gln Thr
50 55 60

Lys Arg His Gln Asp Ala Val Glu Ala Phe Phe Lys Lys Ile Gly Met
65 70 75 80

Asp Tyr Gly Lys Glu Val Glu Phe Pro Ala Phe Val Asp Gly Trp Lys
85 90 95

Glu Leu Ala Asn Tyr Asp Leu Lys Leu Trp Ser Gln Asn Lys Lys Ser
100 105 110

Leu Ile Arg Asp Trp Gly Glu Ala Val Phe Asp Ile Phe Asp Lys Asp
115 120 125

Gly Ser Gly Ser Ile Ser Leu Asp Glu Trp Lys Ala Tyr Gly Arg Ile
130 135 140

Ser Gly Ile Cys Ser Ser Asp Glu Asp Ala Glu Lys Thr Phe Lys His
145 150 155 160

Cys Asp Leu Asp Asn Ser Gly Lys Leu Asp Val Asp Glu Met Thr Arg
165 170 175

Gln His Leu Gly Phe Trp Tyr Thr Leu Asp Pro Asn Ala Asp Gly Leu
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Tyr Gly Asn Phe Val Pro
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<212> PRT

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Asp Ile Asn Gly Asp Gly Lys Ile Thr Leu Asp Glu Ile Val Ser Lys
        35                  40                  45

Ala Ser Asp Asp Ile Cys Ala Lys Leu Glu Ala Thr Pro Glu Gln Thr
    50                  55                  60

Lys Arg His Gln Val Cys Val Glu Ala Phe Phe Arg Gly Cys Gly Met
65                  70                  75                  80

Glu Tyr Gly Lys Glu Ile Ala Phe Pro Gln Phe Leu Asp Gly Trp Lys
                85                  90                  95

Gln Leu Ala Thr Ser Glu Leu Lys Lys Trp Ala Arg Asn Glu Pro Thr
            100                 105                 110

Leu Ile Arg Glu Trp Gly Asp Ala Val Phe Asp Ile Phe Asp Lys Asp
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Gly Ser Gly Ser Ile Ser Leu Asp Glu Trp Lys Ala Tyr Gly Arg Ile
    130                 135                 140

Ser Gly Ile Cys Ser Ser Asp Glu Asp Ala Glu Lys Thr Phe Lys His
145                 150                 155                 160

Cys Asp Leu Asp Asn Ser Gly Lys Leu Asp Val Asp Glu Met Thr Arg
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Gln His Leu Gly Phe Trp Tyr Thr Leu Asp Pro Asn Ala Asp Gly Leu
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Tyr Gly Asn Phe Val Pro
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cccgagcaga ccaagagaca ccaggacgcc gtggaggcct tcttcaagaa gatcggcatg 240

gactacggca aggaggtgga gttccccgcc ttcgtggacg gctggaagga gctggccaac 300

taccacctga agctgtggag ccagaacaag aagagcctca tcagggactg gggcgaggcc 360

gtgttcgaca tcttcgacaa ggacggcagc ggctgcatca gcctggatga gtggaaggcc 420

tacggcagaa tcagcggcat ctgcagcagc gacgaggacg ccgaaaagac cttcaagcac 480

tgcgacctgg acaacagcgg caagctggac gtggacgaga tgaccagaca gcacctggac 540

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<211> 600

<212> DNA

<213> Unknown

<220>

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accctggacg agatcgtgag caaggccagc gacgacatct gcgccaagct gggcgccacc 180

cccgagcaga ccaagagaca ccaggacgcc gtggaggcct tcttcaagaa gatcggcatg 240

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tacgacctga agctgtggag ccagaacaag aagagcctca tcagggactg gggcgaggcc 360

gtgttcgaca tcttcgacaa ggacggcagc ggctgcatca gcctggatga gtggaaggcc 420

tacggcagaa tcagcggcat ctgcagcagc gacgaggacg ccgaaaagac cttcaagcac 480

tgcgacctgg acaacagcgg caagctggac gtggacgaga tgaccagaca gcacctgggc 540

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<211> 600

<212> DNA

<213> Unknown

<220>

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accctggacg agatcgtgag cagggccagc gacgacatct gcgccaagct gggcgccacc 180

cccgagcaga ccaagagaca ccaggacgcc gtggaggcct tcttcaagaa gatcggcatg 240

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gtgttcgaca tcttcgacaa ggacggcagc ggcagcatca gcctggatga gtggaaggcc 420

tacggcagaa tcagcggcat ctgcagcagc gacgaggacg ccgaaaagac cttcaagcac 480

tgcgacctgg acaacagcgg caagctggac gtggacgaga tgaccagaca gcacctgggc 540

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<211> 600

<212> DNA

<213> Unknown

<220>

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accctggacg agatcgtgag caaggccagc gacgacatct gcgccaagct gggcgccacc 180

cccgagcaga ccaagagaca ccgggacgcc gtggaggcct tcttcaagaa gatcggcatg 240

gactacggca aggaggtgga gttccccgtc ttcgtggacg gctggaagga gctggccaac 300

tacgacctga agctgtggag ccagaacaag aagagcctca tcagggactg gggcgaggcc 360

gtgtttgaca tcttcgacaa ggacggcagc ggcagcatta gcctggatga gtggaaggcc 420

tacggtagaa tcagcggcat ctgcagcagc gacgaggacg ccgaaaagac cttcaagcac 480

tgcgacctgg acaacagcgg caagctggac gtggacgaga tgaccagaca gcacctgggc 540

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<211> 600

<212> DNA

<213> Unknown

<220>

<223> Clytin mutant: 1C12 mutant_dna

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accctggacg agatcgtgag caaggccagc gacgacatct gcgccaagct gggcgccacc 180

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gtgttcgaca tcctcgacaa ggacggcagc ggcagcatca gcctggatga gtggaaggcc 420

tacggcagaa tcagcggcat ctgcagaagc gacgaggacg ccgaaaagac cttcaagcac 480

tgcgacctgg acaacagcgg caagctggac gtggacgaga tgaccagaca gcacctgggc 540

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<211> 600

<212> DNA

<213> Unknown

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accctggacg agatcgtgag caaggccagc gacgacatct gcgccaagct gggcgccacc 180

cccgagcaga ccaagagaca ccaggacgcc gtggaggcct tcttcaagaa gatcggcatg 240

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tacgacctga agctgtggag ccagaacaag aagagcctca tcagggactg gggcgaggcc 360

gtgttcgaca tcttcgacaa ggacggcagc ggcagcatca gcctggatga gtggaaggcc 420

tactgcagaa tcagcggcat ctgcagcagc gacgaggacg ccgaaaagac cttcaagcac 480

tgcgacctgg acaacagcgg caagctggac gtggacgaga tgaccagaca gcacctgggc 540

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<211> 600

<212> DNA

<213> Unknown

<220>

<223> Clytin mutant: 3C12 mutant_dna

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accctggacg agatcgtgag caaggccagc gacgacgtct gcgccaagct gggcgccacc 180

cccgagcaga ccaagagaca ccaggacgcc gtggaggcct tcttcaagaa gatcggcatg 240

gactacggca aggaggtgga gttccccgcc ttcgtggacg gctggaagga gctggccaac 300

tacgacctga agctgtggag ccaaaacaag aagagcctca tcagggactg gggcgaggcc 360

gtgttcgaca tcttcgacaa ggacggcagc ggcagcatca gcctggacga gtggaaggcc 420

tacggcagaa tcagcggcat ctgcagaagc gacgaggacg ccgaaaagac cttcaagcac 480

tgcgacctgg acaacagcgg caagctggac gtggacgaga tgaccagaca gcacctgggc 540

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<211> 600

<212> DNA

<213> Unknown

<220>

<223> Clytin mutant: 6H22 mutant_dna

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accctggacg agatcgtgag caaggccagc gacgacatct gcgccaggct gggcgccacc 180

cccgagcaga ccaagagaca ccaggacgcc gtggaggcct tcttcaagaa gatcggcatg 240

gactacggca aagaggtgga gttccccgcc ttcgtggacg gctggaagga gctggccaac 300

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gtgttcgaca tcttcgacaa ggacggcagc ggcagcatca gcctggatga gtggaaggcc 420

tacggcagaa tcagcggcat ctgcagcagc gacgaggacg ccgaaaagac cttcaagcac 480

tgcgacctgg acaacagcgg caagctggac gtggacgaga tgaccagaca gcacctgggc 540

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<211> 597

<212> DNA

<213> Unknown

<220>

<223> Clytin mutant: 12mutCly_dna

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accctggacg agatcgtgag caaggccagc gacgacatct gcgccaagct ggaggccacc 180

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<211> 32

<212> DNA

<213> Unknown

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<211> 33

<212> DNA

<213> Unknown

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<210> 24

<211> 99

<212> DNA

<213> Homo sapiens

<400> 24

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